GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2005, 12:01:52 ; Search time 39 Seconds
(without alignments)
244.243 Million cell updates/sec

Title: US-09-941-997-2
Perfect score: 495
Sequence: 1 MADGSSDAAREPRPAPAPIR.....CQPLELAGLGFAELQDLCRQ 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	495	100.0	210	1	TPHUIC	troponin I, cardia
2	441.5	89.2	211	1	TPRBIC	troponin I, cardia
3	440.5	89.0	211	2	A53805	troponin I, cardia
4	438.5	88.6	211	2	A60124	troponin I, cardia
5	435.5	88.0	211	2	I56441	troponin I - rat
6	413	83.4	211	2	A29994	troponin I, cardia
7	301.5	60.9	208	2	A41030	troponin I, cardia
8	294.5	59.5	244	2	I51408	cardiac troponin I
9	164	33.1	187	2	B44786	troponin I, slow s
10	154	31.1	187	1	TPHUIW	troponin I, slow s
11	142	28.7	184	1	TPRBIW	troponin I, slow s
12	129.5	26.2	182	1	TPRBIS	troponin I, fast s
13	129.5	26.2	182	2	A44786	troponin I, fast s
14	126.5	25.6	182	1	TPHUIS	troponin I, fast s
15	122.5	24.7	142	2	JC5612	troponin I beta -
16	121.5	24.5	142	2	JC5611	troponin I alpha -
17	120.5	24.3	208	2	A40547	troponin I - fruit
18	119.5	24.1	183	1	TPCHIS	troponin I, fast s
19	119.5	24.1	183	2	A23569	troponin I, fast s
20	118.5	23.9	173	2	JC5610	troponin I - sea s
21	113.5	22.9	260	2	B38594	troponin I - fruit
22	109.5	22.1	201	2	A31484	troponin I, fast s
23	103.5	20.9	208	2	A38594	troponin I - fruit
24	96.5	19.5	176	2	S70008	troponin I - Atlan
25	86.5	17.5	260	2	T25017	hypothetical prote
26	82.5	16.7	292	2	JE0233	troponin-I - scall
27	74.5	15.1	742	2	T38001	probable phosphati
28	74	14.9	233	2	T17218	hypothetical prote
29	73.5	14.8	327	2	S49619	crtA protein - Rho
30	72.5	14.6	335	2	T33457	hypothetical prote
31	72.5	14.6	338	2	I53043	transforming prote
32	72	14.5	886	2	S07132	hypothetical prote
33	72	14.5	1415	1	EDBEGA	immediate-early pr
34	71.5	14.4	306	2	T27985	hypothetical prote
35	71.5	14.4	324	2	F64592	hypothetical prote
36	71.5	14.4	351	2	B34768	ORF5 protein - Orf
37	71	14.3	197	2	T15106	hypothetical prote
38	70.5	14.2	314	2	JC4951	troponin T - scall
39	70.5	14.2	327	2	T50744	spheroidene monoox
40	70.5	14.2	387	2	S02708	troponin T - fruit
41	70.5	14.2	462	2	T46215	hypothetical prote
42	70	14.1	303	2	A48130	growth arrest-spec
43	70	14.1	2957	2	T33152	hypothetical prote
44	69.5	14.0	263	2	A34466	calpain (EC 3.4.22
45	69.5	14.0	344	2	F98307	hypothetical prote

ALIGNMENTS

RESULT 1
TPHUIC
troponin I, cardiac muscle - human
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: A61229; JN0837; S11522; A33185; S63690
R;Hunkeler, N.M.; Kullman, J.; Murphy, A.M.
Circ. Res. 69: 1409-1414 (1991)
A;Title: Troponin I isoform expression in human heart.
A;Reference number: A61229; MUID:92035427; PMID:1934363
A;Accession: A61229
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-210 <HUN>
A;Cross-references: UNIPROT:P19429
R;Armour, K.L.; Harris, W.J.; Tempest, P.R.
Gene 131: 287-292 (1993)
A;Title: Cloning and expression in Escherichia coli of the cDNA encoding human cardiac
A;Reference number: JN0837; MUID:94010323; PMID:8406024
A;Accession: JN0837
A;Molecule type: mRNA
A;Residues: 1-210 <AR2>
A;Cross-references: GB:M64247; NID:g339966; PIDN:AAA16157.1; PID:g339967
R;Vallins, W.J.; Brand, N.J.; Dabhade, N.; Butler-Browne, G.; Yacoub, M.H.; Barton, P.J
FEBS Lett. 270: 57-61 (1990)
A;Title: Molecular cloning of human cardiac troponin I using polymerase chain reaction.
A;Reference number: S11522; MUID:91032031; PMID:2226790
A;Accession: S11522
A;Molecule type: mRNA
A;Residues: 1-85,'T',87-210 <VAL>
A;Cross-references: EMBL:X54163; NID:g37427; PIDN:CAA38102.1; PID:g37428
R;Mittmann, K.; Jaquet, K.; Heilmeyer Jr., L.M.G.
FEBS Lett. 273: 41-45 (1990)
A;Title: A common motif of two adjacent phosphoserines in bovine, rabbit and human card
A;Reference number: S12886; MUID:91032199; PMID:2226863
A;Contents: annotation; acetylated amino end; phosphorylation sites
C;Genetics:
A;Gene: GDB:TNNI3
A;Cross-references: GDB:125309; OMIM:191044
A;Map position: 19p13.2-19q13.2
C;Complex: troponin is a heterotrimer with one molecule each of troponin C (calcium bin
C;Function:
A;Description: binds actin and inhibits myosin ATPase activity; with tropomyosin mediat
A;Pathway: muscle contraction
C;Superfamily: troponin I
C;Keywords: acetylated amino end; actin binding; cardiac muscle; heart; muscle contract
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;23,24/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status exp

Query Match 100.0%; Score 495; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 3.3e-39;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99


RESULT 2
TPRBIC
troponin I, cardiac muscle - rabbit (tentative sequence)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: A90296; A90294; S12886; A03090
R;Grand, R.J.A.; Wilkinson, J.M.
Biochem. J. 167, 183-192, 1977
A;Title: The amino acid sequence of rabbit slow-muscle troponin I.
A;Reference number: A90296; MUID:78060292; PMID:588250
A;Accession: A90296
A;Molecule type: protein
A;Residues: 1-4,'R',6-16,18-20,22,'D',27-211 <GRA>
A;Cross-references: UNIPROT:P02646
R;Grand, R.J.A.; Wilkinson, J.M.; Mole, L.E.
Biochem. J. 159, 633-641, 1976
A;Title: The amino acid sequence of rabbit cardiac troponin I.
A;Reference number: A90294; MUID:77087072; PMID:1008822
A;Accession: A90294
A;Molecule type: protein
A;Residues: 1-4,'R',6-11,'K',13-16,18-20,22,'D',27-211 <GR2>
R;Mittmann, K.; Jaquet, K.; Heilmeyer Jr., L.M.G.
FEBS Lett. 273, 41-45, 1990
A;Title: A common motif of two adjacent phosphoserines in bovine, rabbit and human cardi
A;Reference number: S12886; MUID:91032199; PMID:2226863
A;Accession: S12886
A;Molecule type: protein
A;Residues: 1-36 <MIT>
A;Note: peptide sequences corrected; amino terminal acetylation; phosphorylation sites
R;Solaro, R.J.; Moir, A.J.G.; Perry, S.V.
Nature 262, 615-617, 1976
A;Title: Phosphorylation of troponin I and the inotropic effect of adrenaline in the per
A;Reference number: A93181; MUID:76267707; PMID:958429
A;Contents: annotation; phosphorylation sites
C;Complex: troponin is a heterotrimer with one molecule each of troponin C (calcium bind
C;Function:
A;Description: binds actin and inhibits myosin ATPase activity; with tropomyosin mediate
A;Pathway: muscle contraction
C;Superfamily: troponin I
C;Keywords: acetylated amino end; actin binding; cardiac muscle; heart; muscle contracti
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;22,23/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status expe

  Query Match             89.2%;  Score 441.5;  DB 1;  Length 211;
  Best Local Similarity   90.9%;  Pred. No. 3.4e-34;
  Matches   90;  Conservative    3;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          2 ADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              || |:||| | ||||||:||||| |||||||||||| | |||||||||||||:|||||||
Db          1 ADESTDAAGEARPAPAPVRRRSSANYRAYATEPHAKSKKKISASRKLQLKTLMLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99


RESULT 3
A53805
troponin I, cardiac - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: A53805; A53108
R;Guo, X.; Wattanapermpool, J.; Palmiter, K.A.; Murphy, A.M.; Solaro, R.J.
J. Biol. Chem. 269, 15210-15216, 1994
A;Title: Mutagenesis of cardiac troponin I. Role of the unique NH-2-terminal peptide in
A;Reference number: A53805; MUID:94253083; PMID:8195157
A;Accession: A53805
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-211 <GUO>
A;Cross-references: UNIPROT:P48787; GB:U09181; NID:g484093; PIDN:AAA19657.1; PID:g508866
R;Ausoni, S.; Campione, M.; Picard, A.; Moretti, P.; Vitadello, M.; De Nardi, C.; Schiaf
J. Biol. Chem. 269, 339-346, 1994
A;Title: Structure and regulation of the mouse cardiac troponin I gene.
A;Reference number: A53108; MUID:94103233; PMID:8276817
A;Accession: A53108
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-211 <RES>
A;Cross-references: EMBL:Z22784; NID:g313104; PIDN:CAA80459.1; PID:g313105
C;Genetics:
A;Introns: 4/2; 8/3; 37/3; 51/3; 95/3; 125/3; 184/3
C;Superfamily: troponin I
C;Keywords: actin binding; cardiac muscle; heart; phosphoprotein

  Query Match             89.0%;  Score 440.5;  DB 2;  Length 211;
  Best Local Similarity   89.0%;  Pred. No. 4.2e-34;
  Matches   89;  Conservative    4;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 MADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQ 59
              ||| ||||| ||:|||||:||||| |||||||||||||||||||||||||:|||||||
Db          1 MADESSDAAGEPQPAPAPVRRRSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQ 60

Qy         60 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |:|||||||||||| | |||||||| |||| ||||||||
Db         61 EMEREAEERRGEKGRVLRTRCQPLELDGLGFEELQDLCRQ 100


RESULT 4
A60124
troponin I, cardiac muscle - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60124; A38398; S14849
R;Ausoni, S.; De Nardi, C.; Moretti, P.; Gorza, L.; Schiaffino, S.
Development 112, 1041-1051, 1991
A;Title: Developmental expression of rat cardiac troponin I mRNA.
A;Reference number: A60124; MUID:92037196; PMID:1935696
A;Accession: A60124
A;Molecule type: mRNA
A;Residues: 1-211 <AUS>
A;Cross-references: UNIPROT:P23693; EMBL:X58499; NID:g56022; PIDN:CAA41402.1; PID:g56023
R;Murphy, A.M.; Jones II, L.; Sims, H.F.; Strauss, A.W.
Biochemistry 30, 707-712, 1991
A;Title: Molecular cloning of rat cardiac troponin I and analysis of troponin I isoform
A;Reference number: A38398; MUID:91105162; PMID:1988058
A;Accession: A38398
A;Molecule type: mRNA
A;Residues: 1-211 <MUR>
A;Cross-references: GB:M57679; GB:J05304; NID:g207509; PIDN:AAA63504.1; PID:g207510
C;Superfamily: troponin I
C;Keywords: actin binding; cardiac muscle; heart

  Query Match             88.6%;  Score 438.5;  DB 2;  Length 211;
  Best Local Similarity   89.0%;  Pred. No. 6.4e-34;
  Matches   89;  Conservative    4;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 MADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQ 59
              ||| ||||| ||:|||||:||||| |||||||||||||||||||||||||:|||||||
Db          1 MADESSDAAGEPQPAPAPVRRRSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQ 60

Qy         60 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |:|||||||||||| |||||||| | |||| ||||||||
Db         61 EMEREAEERRGEKGRVLSTRCQPLVLDGLGFEELQDLCRQ 100
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RESULT 5
I56441
troponin I - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56441
R;Martin, A.F.; Orlowski, J.
J. Mol. Cell. Cardiol. 23, 583-588, 1991
A;Title: Molecular cloning and developmental expression of the rat cardiac-specific isof
A;Reference number: I56441; MUID:91359315; PMID:1886137
A;Accession: I56441
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-211 <RES>
A;Cross-references: UNIPROT:P23693; GB:M92074; NID:g207515; PIDN:AAA42294.1; PID:g207516
C;Superfamily: troponin I

  Query Match             88.0%;  Score 435.5;  DB 2;  Length 211;
  Best Local Similarity   88.0%;  Pred. No. 1.2e-33;
  Matches   88;  Conservative    5;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 MADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQ 59
              ||| |||:| ||:|||||:||||| ||||||||||||||||||||||||||||:||||||
Db          1 MADESSDSAGEPQPAPAPVRRRSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQ 60

Qy         60 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |:|||||||||||||.|||||||| | |||| ||||||||
Db         61 EMEREAEERRGEKGRVLSTRCQPLVLDGLGFEELQDLCRQ 100


RESULT 6
A29994
troponin I, cardiac muscle - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29994; S02628
R;Leszyk, J.; Dumaswala, R.; Potter, J.D.; Collins, J.H.
Biochemistry 27, 2821-2827, 1988
A;Title: Amino acid sequence of bovine cardiac troponin I.
A;Reference number: A29994; MUID:88294022; PMID:3042023
A;Accession: A29994
A;Molecule type: protein
A;Residues: 1-211 <LES>
A;Cross-references: UNIPROT:P08057
R;Swiderek, K.; Jaquet, K.; Meyer, H.E.; Heilmeyer Jr., L.M.G.
Eur. J. Biochem. 176, 335-342, 1988
A;Title: Cardiac troponin I, isolated from bovine heart, contains two adjacent phosphose
A;Reference number: S02628; MUID:88329087; PMID:3138117
A;Accession: S02628
A;Molecule type: protein
A;Residues: 21-27,'Y',28-37 <SWI>
A;Note: authors comment in a note added in proof that the extra tyrosine is an error
C;Superfamily: troponin I
C;Keywords: acetylated amino end; actin binding; cardiac muscle; heart; muscle; phosphop
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;23,24/Binding site: phosphate (Ser) (covalent) #status experimental

  Query Match             83.4%;  Score 413;  DB 2;  Length 211;
  Best Local Similarity   87.0%;  Pred. No. 1.6e-31;
  Matches   87;  Conservative    3;  Mismatches    8;  Indels    2;  Gaps    2;

Qy          2 ADGS-SDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQ 59
              || |    | :  ||| |:||||| ||||||||||||||||||||||||||||:||||||
Db          1 ADRSGGSTAGDTVPAPPPVRRRSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQ 60

Qy         60 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||||
Db         61 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 100


RESULT 7
A41030
troponin I, cardiac muscle - quail
C;Species: Coturnix coturnix (quail)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Aug-1999
C;Accession: A41030
R;Hastings, K.E.M.; Koppe, R.I.; Marmor, E.; Bader, D.; Shimada, Y.; Toyota, N.
J. Biol. Chem. 266, 19659-19665, 1991
A;Title: Structure and developmental expression of troponin I isoforms. cDNA clone anal
A;Reference number: A41030; MUID:92011768; PMID:1918073
A;Accession: A41030
A;Molecule type: mRNA
A;Residues: 1-208 <HAS>
A;Cross-references: GB:M73702; NID:g213647; PIDN:AAA49513.1; PID:g213648
C;Superfamily: troponin I
C;Keywords: actin binding; cardiac muscle; heart

  Query Match             60.9%;  Score 301.5;  DB 2;  Length 208;
  Best Local Similarity   67.4%;  Pred. No. 4.1e-21;
  Matches   62;  Conservative   10;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          9 AREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQELEREAEE 67
              | |  | | |:||:|| ||| || ||||||::||||||||||||||||| ||::|||| :|
Db          2 AEEEEPKPPPLRRKSSANYRGYAVEPHAKRQSKISASRKLQLKTLLLQRAKRDLEREEQE 61

Qy         68 RRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              | ||| | |   | | || ||| |:||:|||:
Db         62 RAGEKQRHLGELCPPPELDGLGVAQLQELCRE 93


RESULT 8
I51408
cardiac troponin I - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51408
R;Drysdale, T.A.; Tonissen, K.F.; Patterson, K.D.; Crawford, M.J.; Krieg, P.A.
Dev. Biol. 165, 432-441, 1994
A;Title: Cardiac troponin I is a heart-specific marker in the Xenopus embryo: expressic
A;Reference number: I51408; MUID:95046865; PMID:7958411
A;Accession: I51408
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-244 <DRY>
A;Cross-references: UNIPROT:P50754; GB:L25721; NID:g410050; PIDN:AAA65727.1; PID:g41005
C;Superfamily: troponin I
C;Keywords: cardiac muscle; heart

  Query Match             59.5%;  Score 294.5;  DB 2;  Length 244;
  Best Local Similarity   62.6%;  Pred. No. 2.2e-20;
  Matches   62;  Conservative   12;  Mismatches   18;  Indels    7;  Gaps    2;

Qy          8 AAREPRPAPAP------IRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              |    |:||| |      |||||| |||:|||||  |:| |||||||||| |::|||||
Db         26 APEPPKPAPPPAAPPPLIRRRSSANYRSYATEPQVKRKPKISASRKLQLNTMMLQIAKAE 85

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              :||| |||  || | |:  ||||:|:||  :||||||::
Db         86 MEREEEERAREKERYLAEHCQPLQLSGLSRSELQDLCQE 124


RESULT 9
B44786
troponin I, slow skeletal muscle - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C;Accession: B44786
R;Koppe, R.I.; Hallauer, P.L.; Karpati, G.; Hastings, K.E.M.
J. Biol. Chem. 264, 14327-14333, 1989
A;Title: cDNA clone and expression analysis of rodent fast and slow skeletal muscle trc
A;Reference number: A44786; MUID:89340548; PMID:2760067
A;Accession: B44786
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-187 <KOP>
A;Cross-references: UNIPROT:P13413; GB:J04993; NID:g207517; PIDN:AAA42295.1; PID:g20751
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C;Superfamily: troponin I
C;Keywords: skeletal muscle

  Query Match           33.1%;  Score 164;  DB 2;  Length 187;
  Best Local Similarity   53.7%;  Pred. No. 2.7e-08;
  Matches   36;  Conservative   10;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         33 PHAKKKSKISASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPLELAGLGFAE 92
              |  ::||||:||||| ||:|:|  ||:  |:| ||| || | || |   |:  ||  :
Db          2 PEVERKSKITASRKLMLKSLMLAKAKECWEQEHEEREAEKVRYLSERIPTLQTRGLSLSA 61

Qy         93 LQDLCRQ 99
              |||||:
Db         62 LQDLCRE 68


RESULT 10
TPHUIW
troponin I, slow skeletal muscle - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: A53740; A35355
R;Corin, S.J.; Juhasz, O.; Zhu, L.; Conley, P.; Kedes, L.; Wade, R.
J. Biol. Chem. 269, 10651-10659, 1994
A;Title: Structure and expression of the human slow twitch skeletal muscle troponin I ge
A;Reference number: A53740; MUID:94193765; PMID:8144655
A;Accession: A53740
A;Molecule type: DNA
A;Residues: 1-187 <COR>
A;Cross-references: UNIPROT:P19237; GB:L21905
R;Wade, R.; Eddy, R.; Shows, T.B.; Kedes, L.
Genomics 7, 346-357, 1990
A;Title: cDNA sequence, tissue-specific expression, and chromosomal mapping of the human
A;Reference number: A35355; MUID:90307007; PMID:2365354
A;Accession: A35355
A;Molecule type: mRNA
A;Residues: 1-181,'NA',184-187 <WAD>
A;Cross-references: GB:J04760; NID:g339964; PIDN:AAA61228.1; PID:g339965
C;Genetics:
A;Gene: GDB:TNNI1
A;Cross-references: GDB:120443; OMIM:191042
A;Map position: 1q32-1q32
A;Introns: 4/2; 1/3; 19/3; 63/3; 93/3; 152/3
A;Note: the first intron occurs before the initiator codon
C;Complex: troponin is a heterotrimer with one molecule each of troponin C (calcium bind
C;Function:
A;Description: binds actin and inhibits myosin ATPase activity; with tropomyosin mediate
A;Pathway: muscle contraction
C;Superfamily: troponin I
C;Keywords: acetylated amino end; actin binding; muscle contraction; skeletal muscle
F;2/Modified site: acetylated amino end (Pro) (in mature form) #status predicted

  Query Match           31.1%;  Score 154;  DB 1;  Length 187;
  Best Local Similarity   50.7%;  Pred. No. 2.4e-07;
  Matches   34;  Conservative   11;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         33 PHAKKKSKISASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPLELAGLGFAE 92
              |  ::| ||:||||| ||:|:|  ||:  |:| |||  || | |: |   |:  ||  :
Db          2 PEVERKPKITASRKLLLKSLMLAKAKECWEQEHEEREAEKVRYLAERIPTLQTRGLSLSA 61

Qy         93 LQDLCRQ 99
              |||||:
Db         62 LQDLCRE 68


RESULT 11
TPRBIW
troponin I, slow skeletal muscle - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Apr-1979 #sequence_revision 30-Apr-1979 #text_change 09-Jul-2004
C;Accession: A03089
R;Grand, R.J.A.; Wilkinson, J.M.
Biochem. J. 167, 183-192, 1977
A;Title: The amino acid sequence of rabbit slow-muscle troponin I.
A;Reference number: A90296; MUID:78060292; PMID:588250
A;Accession: A03089
A;Molecule type: protein
A;Residues: 1-184 <GRA>
A;Cross-references: UNIPROT:P02645
A;Note: some of the molecules lack residues 183 and 184
C;Complex: troponin is a heterotrimer with one molecule each of troponin C (calcium binc
C;Function:
A;Description: binds actin and inhibits myosin ATPase activity; with tropomyosin mediate
A;Pathway: muscle contraction
C;Superfamily: troponin I
C;Keywords: actin binding; blocked amino end
F;1/Modified site: blocked amino end (Pro) (partial) (probably acetylated) #status expe

  Query Match           28.7%;  Score 142;  DB 1;  Length 184;
  Best Local Similarity   52.2%;  Pred. No. 3.1e-06;
  Matches   35;  Conservative   10;  Mismatches   20;  Indels    2;  Gaps    2;

Qy         33 PHAKKKSKISASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPLELAGLGFAE 92
              |  ::||||:||||| ||:|:|  || | ::| | |  || | |: |   |:  ||  :
Db          1 PEVERKSKITASRKL-LKSLMLAKAK-ECQQEHEAREAEKVRYLAERIPALQTRGLSLSA 58

Qy         93 LQDLCRQ 99
              |||||||
Db         59 LQDLCRQ 65


RESULT 12
TPRBIS
troponin I, fast skeletal muscle - rabbit
N;Alternate names: TnI
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: A45060; A93193; A90286; I46514; A03087
R;Sheng, Z.; Pan, B.S.; Miller, T.E.; Potter, J.D.
J. Biol. Chem. 267, 25407-25413, 1992
A;Title: Isolation, expression, and mutation of a rabbit skeletal muscle cDNA clone for
A;Reference number: A45060; MUID:93094259; PMID:1339446
A;Accession: A45060
A;Molecule type: mRNA
A;Residues: 1-46,'DS',49-182 <SHE>
A;Cross-references: UNIPROT:P02643; GB:L04347
A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIP:120236) and corrected to correspond
A;Note: the authors translated the codons GGC for residue 56 as Gln, and TAT for residue
R;Wilkinson, J.M.; Grand, R.J.A.
Nature 271, 31-35, 1978
A;Title: Comparison of amino acid sequence of troponin I from different striated muscles
A;Reference number: A93193; MUID:78114026; PMID:146828
A;Accession: A93193
A;Molecule type: protein
A;Residues: 2-154,158-182 <WIL>
R;Wilkinson, J.M.; Grand, R.J.A.
Biochem. J. 149, 493-496, 1975
A;Title: The amino acid sequence of troponin I from rabbit skeletal muscle.
A;Reference number: A90286; MUID:76039510; PMID:1180911
A;Accession: A90286
A;Molecule type: protein
A;Residues: 2-114,'R4,115-154,158-182 <WI2>
R;Moir, A.J.G.; Wilkinson, J.M.; Perry, S.V.
FEBS Lett. 42, 253-256, 1974
A;Title: The phosphorylation sites of troponin I from white skeletal muscle of the rabbi
A;Reference number: A91408; MUID:74309023; PMID:4369337
A;Contents: annotation; phosphorylation sites
R;Huang, T.S.; Bylund, D.B.; Stull, J.T.; Krebs, E.G.
FEBS Lett. 42, 249-252, 1974
A;Title: The amino acid sequences of the phosphorylated sites in troponin-I from rabbit
A;Reference number: A91407; MUID:74308154; PMID:4369265
A;Contents: annotation; phosphorylation sites
R;Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
A;Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by sho
```

```
A;Reference number: I46471; MUID:83167564; PMID:6687628
A;Accession: I46514
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 166-178 <PUT>
A;Cross-references: EMBL:V00898; NID:g1738; PIDN:CAA24263.1; PID:g929767
C;Complex: troponin is a heterotrimer with one molecule each of troponin C (calcium bind
C;Function:
A;Description: binds actin and inhibits myosin ATPase activity; with tropomyosin mediate
A;Pathway: muscle contraction
C;Superfamily: troponin I
C;Keywords: acetylated amino end; actin binding; muscle contraction; phosphoprotein; ske
F;2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental
F;12/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status experim
F;20,90,118/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status

  Query Match             26.2%;  Score 129.5;  DB 1;  Length 182;
  Best Local Similarity   42.2%;  Pred. No. 4.5e-05;
  Matches   27;  Conservative   14;  Mismatches   22;  Indels    1;  Gaps    1;

Qy         36 KKKSKISASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPLELAGLGFAELQD 95
              :|:::   :|:  ||:::|||| |||:|   |  ||   |: | || | |   ||:|:
Db          5 EKRNRAITARRQHLKSVMLQIAATELEKEEGRREAEKQNYLAEHCPPLSLPG-SMAEVQE 63

Qy         96 LCRQ 99
              ||:|
Db         64 LCKQ 67


RESULT 13
A44786
troponin I, fast skeletal muscle - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C;Accession: A44786
R;Koppe, R.I.; Hallauer, P.L.; Karpati, G.; Hastings, K.E.M.
J. Biol. Chem. 264, 14327-14333, 1989
A;Title: cDNA clone and expression analysis of rodent fast and slow skeletal muscle trop
A;Reference number: A44786; MUID:89340548; PMID:2760067
A;Accession: A44786
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-182 <KOP>
A;Cross-references: UNIPROT:P13412; GB:J04992; NID:g202164; PIDN:AAA40485.1; PID:g202165
C;Superfamily: troponin I
C;Keywords: skeletal muscle

  Query Match             26.2%;  Score 129.5;  DB 2;  Length 182;
  Best Local Similarity   40.6%;  Pred. No. 4.5e-05;
  Matches   26;  Conservative   15;  Mismatches   22;  Indels    1;  Gaps    1;

Qy         36 KKKSKISASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPLELAGLGFAELQD 95
              :|:::   :|:  ||:::|||| |||:|   |  ||   ||  | || : |   :|:|:
Db          5 EKRNRAITARRQHLKSVMLQIAATELEKEESRRESEKENYLSEHCPPLHIPG-SMSEVQE 63

Qy         96 LCRQ 99
              ||:|
Db         64 LCKQ 67


RESULT 14
TPHUIS
troponin I, fast skeletal muscle - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S43508
R;Zhu, L.; Perez-Alvarado, G.; Wade, R.
Biochim. Biophys. Acta 1217, 338-340, 1994
A;Title: Sequencing of a cDNA encoding the human fast-twitch skeletal muscle isoform of
A;Reference number: S43508; MUID:94198300; PMID:8148383
A;Accession: S43508
A;Molecule type: mRNA
A;Residues: 1-182 <ZHU>
A;Cross-references: UNIPROT:P48788; GB:L21715; NID:g452077; PIDN:AAA19813.1; PID:g45207
C;Genetics:
A;Gene: GDB:TNNI2
A;Cross-references: GDB:125308; OMIM:191043
A;Map position: 1q32-1q32
C;Complex: troponin is a heterotrimer with one molecule each of troponin C (calcium bir
C;Function:
A;Description: binds actin and inhibits myosin ATPase activity; with tropomyosin mediat
A;Pathway: muscle contraction
C;Superfamily: troponin I
C;Keywords: acetylated amino end; actin binding; muscle contraction; skeletal muscle
F;2/Modified site: acetylated amino end (Gly) (in mature form) #status predicted

  Query Match             25.6%;  Score 126.5;  DB 1;  Length 182;
  Best Local Similarity   39.1%;  Pred. No. 8.6e-05;
  Matches   25;  Conservative   16;  Mismatches   22;  Indels    1;  Gaps    1;

Qy         36 KKKSKISASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPLELAGLGFAELQD 95
              :|:::   :|:  ||:::|||| |||:|   |  ||   |:  | || : |   :|:|:
Db          5 EKRNRAITARRQHLKSVMLQIAATELEKEESRREAEKQNYLAEHCPPLHIPG-SMSEVQE 63

Qy         96 LCRQ 99
              ||:|
Db         64 LCKQ 67


RESULT 15
JC5612
troponin I beta - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
C;Date: 23-Sep-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: JC5612
R;Yuasa, H.J.; Sato, S.; Yamamoto, H.; Takagi, T.
J. Biochem. 122, 374-380, 1997
A;Title: Primary structure of troponin I isoforms from the ascidian Halocynthia roretzi
A;Reference number: JC5610; MUID:98021076; PMID:9378716
A;Accession: JC5612
A;Molecule type: mRNA
A;Residues: 1-142 <YUA>
A;Cross-references: UNIPROT:O01356; DDBJ:AB001687; NID:g1888348; PIDN:BAA19427.1; PID:g
A;Experimental source: Halocynthia roretzi larva
C;Comment: This protein binds to actin, and inhibits the interaction between actin and
C;Superfamily: troponin I

  Query Match             24.7%;  Score 122.5;  DB 2;  Length 142;
  Best Local Similarity   48.2%;  Pred. No. 0.00016;
  Matches   27;  Conservative   13;  Mismatches   15;  Indels    1;  Gaps    1;

Qy         45 RKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRCQPL-ELAGLGFAELQDLCRQ 99
              ||||||:|||  |:::|:|| |::  || : || | : | :|| :   || :|||:
Db          5 RKLQLKSLLLSRAREDLKREEEQKAEEKKKILSNRIESLGDLASMSQQELMELCRE 60


Search completed: August 30, 2005, 12:12:25
Job time : 41 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2005, 11:53:31 ; Search time 168 Seconds
(without alignments)
301.761 Million cell updates/sec

Title: US-09-941-997-2
Perfect score: 495
Sequence: 1 MADGSSDAAREPRPAPAPIR.....CQPLELAGLGFAELQDLCRQ 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	491	99.2	210	2	Q6FGU5	Q6fgu5 homo sapien
2	490	99.0	209	1	TRIC_HUMAN	P19429 homo sapien
3	443.5	89.6	211	2	Q8MKD5	Q8mkd5 canis famil
4	439.5	88.8	211	1	TRIC_RABIT	P02646 oryctolagus
5	435.5	88.0	210	1	TRIC_MOUSE	P48787 mus musculu
6	435	87.9	210	2	Q863B6	Q863b6 felis silve
7	433.5	87.6	210	1	TRIC_RAT	P23693 rattus norv
8	413	83.4	211	1	TRIC_BOVIN	P08057 bos taurus
9	305.5	61.7	208	2	Q6S7R4	Q6s7r4 meleagris g
10	305.5	61.7	208	2	Q6S7R5	Q6s7r5 meleagris g
11	305.5	61.7	208	2	Q6S7R6	Q6s7r6 gallus gall
12	301.5	60.9	207	1	TRIC_COTJA	P27672 coturnix co
13	296.5	59.9	246	2	Q63ZJ0	Q63zj0 xenopus lae
14	294.5	59.5	243	1	TRIC_XENLA	P50754 xenopus lae
15	293.5	59.3	238	2	Q6YA69	Q6ya69 rana catesb
16	175	35.4	168	1	TRIC_CHICK	P27673 gallus gall
17	166	33.5	198	2	Q6DHL8	Q6dhl8 brachydanio
18	164	33.1	186	1	TRIS_MOUSE	Q9wuz5 mus musculu
19	164	33.1	186	1	TRIS_RAT	P13413 rattus norv
20	163.5	33.0	188	2	Q90350	Q90350 coturnix co
21	154	31.1	186	1	TRIS_HUMAN	P19237 homo sapien
22	154	31.1	187	2	Q96DT9	Q96dt9 homo sapien
23	154	31.1	187	2	Q6FGW1	Q6fgw1 homo sapien
24	154	31.1	187	2	Q6ICU2	Q6icu2 homo sapien
25	154	31.1	187	2	Q86T57	Q86t57 homo sapien
26	154	31.1	187	2	Q7YSF4	Q7ysf4 sus scrofa
27	151	30.5	108	2	Q95KL2	Q95kl2 capra hircu
28	151	30.5	183	2	Q8QGC5	Q8qgc5 xenopus lae
29	151	30.5	183	2	Q7SYY1	Q7syy1 xenopus lae
30	149	30.1	183	2	Q6P8F9	Q6p8f9 xenopus tro
31	147	29.7	260	2	Q8WPC1	Q8wpc1 halocynthia
32	144	29.1	183	2	Q6GNQ7	Q6gnq7 xenopus lae
33	143	28.9	181	2	Q8AW33	Q8aw33 brachydanio
34	142	28.7	184	1	TRIS_RABIT	P02645 oryctolagus
35	135	27.3	187	2	Q6YA68	Q6ya68 rana catesb
36	133	26.9	180	2	Q6IQ92	Q6iq92 brachydanio
37	130.5	26.4	149	2	O01356	O01356 halocynthia
38	130.5	26.4	182	2	Q8QGC6	Q8qgc6 xenopus lae
39	129.5	26.2	181	1	TRIF_MOUSE	P13412 mus musculu
40	129.5	26.2	181	1	TRIF_RABIT	P02643 oryctolagus
41	129.5	26.2	181	1	TRIF_RAT	P27768 rattus norv
42	127.5	25.8	149	2	Q8WSP5	Q8wsp5 halocynthia
43	126.5	25.6	149	2	O01355	O01355 halocynthia
44	126.5	25.6	181	1	TRIF_HUMAN	P48788 homo sapien
45	126.5	25.6	199	2	Q6IMC7	Q6imc7 drosophila

ALIGNMENTS

RESULT 1
Q6FGU5
ID Q6FGU5 PRELIMINARY; PRT; 210 AA.
AC Q6FGU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TNNI3 protein (Fragment).
GN Name=TNNI3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CR542012; CAG46809.1; -.
DR GO; GO:0030484; C:muscle fiber; IEA.
DR InterPro; IPR001978; Troponin.
DR Pfam; PF00992; Troponin; 1.
FT NON_TER 210 210
SQ SEQUENCE 210 AA; 24019 MW; ECEA9DEAC24A78BD CRC64;

Query Match 99.2%; Score 491; DB 2; Length 210;
Best Local Similarity 99.0%; Pred. No. 3.1e-38;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              ||||||||||||||| |||||||||||||||||||||||
Db         61 LEREAEERRGEKGRVLSTRCQPLELAGLGFAELQDLCRQ 99
```

RESULT 2
TRIC_HUMAN
ID TRIC_HUMAN STANDARD; PRT; 209 AA.
AC P19429;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Troponin I, cardiac muscle.
GN Name=TNNI3; Synonyms=TNNC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```
RC   TISSUE=Heart muscle;
RX   MEDLINE=91032031; PubMed=2226790; DOI=10.1016/0014-5793(90)81234-F;
RA   Vallins W.J., Brand N.J., Dabhade N., Butler-Browne G., Yacoub M.H.,
RA   Barton P.J.R.;
RT   "Molecular cloning of human cardiac troponin I using polymerase chain
RT   reaction.";
RL   FEBS Lett. 270:57-61(1990).
RN   [2]
RP   REVISION TO 85, AND SEQUENCE FROM N.A.
RX   MEDLINE=94010323; PubMed=8406024; DOI=10.1016/0378-1119(93)90308-P;
RA   Armour K.L., Harris W.J., Tempest P.R.;
RT   "Cloning and expression in Escherichia coli of the cDNA encoding human
RT   cardiac troponin I.";
RL   Gene 131:287-292(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92035427; PubMed=1934363;
RA   Hunkeler N.M., Kullman J., Murphy A.M.;
RT   "Troponin I isoform expression in human heart.";
RL   Circ. Res. 69:1409-1414(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96299735; PubMed=8661099; DOI=10.1006/geno.1996.0317;
RA   Bhavsar P.K., Brand N.J., Yacoub M.H., Barton P.J.R.;
RT   "Isolation and characterization of the human cardiac troponin I gene
RT   (TNNI3).";
RL   Genomics 35:11-23(1996).
RN   [5]
RP   PHOSPHORYLATION SITES SER-22 AND SER-23.
RX   MEDLINE=98004271; PubMed=9346285;
RA   Keane N.E., Quirk P.G., Gao Y., Patchell V.B., Perry S.V.,
RA   Levine B.A.;
RT   "The ordered phosphorylation of cardiac troponin I by the cAMP-
RT   dependent protein kinase -- structural consequences and functional
RT   implications.";
RL   Eur. J. Biochem. 248:329-337(1997).
RN   [6]
RP   STRUCTURE BY NMR OF 147-163.
RX   PubMed=10387074; DOI=10.1021/bi9901679;
RA   Li M.X., Spyracopoulos L., Sykes B.D.;
RT   "Binding of cardiac troponin-I147-163 induces a structural opening in
RT   human cardiac troponin-C.";
RL   Biochemistry 38:8289-8298(1999).
RN   [7]
RP   STRUCTURE BY NMR OF 148-164 IN COMPLEX WITH CARDIAC TROPONIN C.
RX   MEDLINE=22172844; PubMed=12060657; DOI=10.1074/jbc.M203896200;
RA   Wang X., Li M.X., Sykes B.D.;
RT   "Structure of the regulatory N-domain of human cardiac troponin C in
RT   complex with human cardiac troponin I147-163 and bepridil.";
RL   J. Biol. Chem. 277:31124-31133(2002).
RN   [8]
RP   VARIANTS CMH7 GLY-144 AND GLN-205.
RX   MEDLINE=97385244; PubMed=9241277;
RA   Kimura A., Harada H., Park J.-E., Nishi H., Satoh M., Takahashi M.,
RA   Hiroi S., Sasaoka T., Ohbuchi N., Nakamura T., Koyanagi T.,
RA   Hwang T.-H., Choo J., Chung K.-S., Hasegawa A., Nagai R., Okazaki O.,
RA   Nakamura H., Matsuzaki M., Sakamoto T., Toshima H., Koga Y.,
RA   Imaizumi T., Sasazuki T.;
RT   "Mutations in the cardiac troponin I gene associated with hypertrophic
RT   cardiomyopathy.";
RL   Nat. Genet. 16:379-382(1997).
RN   [9]
RP   VARIANTS CMH7 SER-81 AND ASN-195.
RX   MEDLINE=21673699; PubMed=11815426; DOI=10.1161/hc0402.102990;
RA   Niimura H., Patton K.K., McKenna W.J., Soults J., Maron B.J.,
RA   Seidman J.G., Seidman C.E.;
RT   "Sarcomere protein gene mutations in hypertrophic cardiomyopathy of
RT   the elderly.";
RL   Circulation 105:446-451(2002).
RN   [10]
RP   VARIANTS RCM GLN-143; TRP-144; THR-170; GLU-177; HIS-189 AND HIS-191.
RX   MEDLINE=22419550; PubMed=12531876;
RA   Mogensen J., Kubo T., Duque M., Uribe W., Shaw A., Murphy R.,
RA   Gimeno J.R., Elliott P., McKenna W.J.;
RT   "Idiopathic restrictive cardiomyopathy is part of the clinical
RT   expression of cardiac troponin I mutations.";
RL   J. Clin. Invest. 111:209-216(2003).
CC   -!- FUNCTION: Troponin I is the inhibitory subunit of troponin, the
CC       thin filament regulatory complex which confers calcium-sensitivity
CC       to striated muscle actomyosin ATPase activity.
CC   -!- SUBUNIT: Binds to actin and tropomyosin.
CC   -!- DISEASE: Defects in TNNI3 are the cause of familial hypertrophic
CC       cardiomyopathy type 7 (CMH7) [MIM:191044]; also known as FHC type
CC       7. CMH7 is an autosomal dominant disorder characterized by
CC       increased myocardial mass with myocyte and myofibrillar disarray.
CC   -!- DISEASE: Defects in TNNI3 are the cause of familial restrictive
CC       cardiomyopathy (RCM) [MIM:115210]. RCM is an heart muscle disorder
CC       characterized by impaired filling of the ventricles with reduced
CC       volume in the presence of normal or near normal wall thickness and
CC       systolic function. The disease may be associated with systemic
CC       disease but is most often idiopathic.
CC   -!- SIMILARITY: Belongs to the troponin I family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54163; CAA38102.1; ALT_SEQ.
DR   EMBL; M64247; AAA16157.1; -.
DR   EMBL; X90780; CAA62301.1; -.
DR   PIR; A61229; TPHUIC.
DR   PDB; 1J1D; X-ray; C/F=30-162.
DR   PDB; 1J1E; X-ray; C/F=30-208.
DR   PDB; 1LXF; NMR; I=147-163.
DR   PDB; 1MXL; NMR; I=147-163.
DR   Genew; HGNC:11947; TNNI3.
DR   MIM; 191044; -.
DR   MIM; 115210; -.
DR   GO; GO:0005861; C:troponin complex; TAS.
DR   GO; GO:0008016; P:regulation of heart rate; TAS.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   3D-structure; Acetylation; Actin-binding; Cardiomyopathy;
KW   Disease mutation; Muscle protein; Phosphorylation.
FT   INIT_MET      0      0
FT   SITE         79     79       Involved in TNI-TNT interactions.
FT   SITE         96     96       Involved in TNI-TNT interactions.
FT   DOMAIN       31     78       Involved in binding TNC.
FT   DOMAIN      128    148       Involved in binding TNC and actin.
FT   MOD_RES       1      1       N-acetylalanine (By similarity).
FT   MOD_RES      22     22       Phosphoserine (by PKA).
FT   MOD_RES      23     23       Phosphoserine (by PKA).
FT   VARIANT      81     81       P -> S (in CMH7).
FT                                /FTId=VAR_016078.
FT   VARIANT     143    143       L -> Q (in RCM).
FT                                /FTId=VAR_016079.
FT   VARIANT     144    144       R -> G (in CMH7).
FT                                /FTId=VAR_007603.
FT   VARIANT     144    144       R -> W (in RCM).
FT                                /FTId=VAR_016080.
FT   VARIANT     170    170       A -> T (in RCM).
FT                                /FTId=VAR_016081.
FT   VARIANT     177    177       K -> E (in RCM).
FT                                /FTId=VAR_016082.
FT   VARIANT     189    189       D -> H (in CMH7 and RCM).
FT                                /FTId=VAR_016083.
FT   VARIANT     191    191       R -> H (in RCM).
FT                                /FTId=VAR_016084.
FT   VARIANT     195    195       D -> N (in CMH7).
FT                                /FTId=VAR_016085.
FT   VARIANT     205    205       K -> Q (in CMH7).
FT                                /FTId=VAR_007604.
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FT   HELIX       151    156
FT   TURN        157    157
SQ   SEQUENCE   209 AA;  23876 MW;  444B82D3DE0467AC CRC64;

  Query Match             99.0%;  Score 490;  DB 1;  Length 209;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-38;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQEL 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQEL 60

Qy         62 EREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 EREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 98


RESULT 3
Q8MKD5
ID   Q8MKD5      PRELIMINARY;      PRT;   211 AA.
AC   Q8MKD5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Cardiac troponin I.
GN   Name=TNNI3;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=23081463; PubMed=14719702;
RA   Rishniw M., Barr S.C., Simpson K.W., Winand N.J., Wootton J.A.;
RT   "Cloning and sequencing of the canine and feline cardiac troponin I
RT   genes.";
RL   Am. J. Vet. Res. 65:53-58(2004).
DR   EMBL; AF506750; AAM33343.1; -.
DR   HSSP; P19429; 1J1D.
DR   GO; GO:0030484; C:muscle fiber; IEA.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
SQ   SEQUENCE   211 AA;  23912 MW;  E26D1FB56C89F9F3 CRC64;

  Query Match             89.6%;  Score 443.5;  DB 2;  Length 211;
  Best Local Similarity   92.0%;  Pred. No. 9.1e-34;
  Matches   92;  Conservative    2;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 MADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQ 59
              ||| | |||  | ||||||||:|| |||||||||||||||||||||||||:||||||
Db          1 MADESGDAAGCPPPAPAPIRRQSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQ 60

Qy         60 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              ||||||||||||||||||||||||||||||||||||||||
Db         61 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 100


RESULT 4
TRIC_RABIT
ID   TRIC_RABIT     STANDARD;      PRT;   211 AA.
AC   P02646;
DT   21-JUL-1986 (Rel. 01, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Troponin I, cardiac muscle.
GN   Name=TNNI3;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77087072; PubMed=1008822;
RA   Grand R.J.A., Wilkinson J.M., Mole L.E.;
RT   "The amino acid sequence of rabbit cardiac troponin I.";
RL   Biochem. J. 159:633-641(1976).
RN   [2]
RP   REVISION.
RX   MEDLINE=78060292; PubMed=588250;
RA   Grand R.J.A., Wilkinson J.M.;
RT   "The amino acid sequence of rabbit slow-muscle troponin I.";
RL   Biochem. J. 167:183-192(1977).
RN   [3]
RP   SEQUENCE OF 1-36, AND PHOSPHORYLATION SITE SER-23.
RC   TISSUE=Heart;
RX   PubMed=2226863;
RA   Mittmann K., Jaquet K., Heilmeyer L.M. Jr.;
RT   "A common motif of two adjacent phosphoserines in bovine, rabbit and
RT   human cardiac troponin I.";
RL   FEBS Lett. 273:41-45(1990).
RN   [4]
RP   PHOSPHORYLATION SITE SER-22.
RX   MEDLINE=76267707; PubMed=958429;
RA   Solaro R.J., Moir A.J.G., Perry S.V.;
RT   "Phosphorylation of troponin I and the inotropic effect of adrenaline
RT   in the perfused rabbit heart.";
RL   Nature 262:615-617(1976).
CC   -!- FUNCTION: Troponin I is the inhibitory subunit of troponin, the
CC       thin filament regulatory complex which confers calcium-sensitivity
CC       to striated muscle actomyosin ATPase activity.
CC   -!- SUBUNIT: Binds to actin and tropomyosin.
CC   -!- PTM: Ser-22 is one of three sites in the region of residues 1-48
CC       that are phosphorylated by phosphorylase kinase.
CC   -!- SIMILARITY: Belongs to the troponin I family.
DR   PIR; A90296; TPRBIC.
DR   HSSP; P19429; 1J1D.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Acetylation; Actin-binding; Direct protein sequencing; Muscle protein;
KW   Phosphorylation.
FT   MOD_RES       1      1       N-acetylalanine (By similarity).
FT   MOD_RES      22     22       Phosphoserine (by PHK).
FT   MOD_RES      23     23       Phosphoserine.
FT   SITE         80     80       Involved in TNI-TNT interactions.
FT   SITE         97     97       Involved in TNI-TNT interactions.
FT   DOMAIN       32     79       Involved in binding TNC.
FT   DOMAIN      129    150       Involved in binding TNC and actin.
FT   CONFLICT      5      5       R -> T (in Ref. 3).
FT   CONFLICT     17     17       Missing (in Ref. 1 and 2).
FT   CONFLICT     21     26       RSSANY -> SD (in Ref. 1 and 2).
SQ   SEQUENCE   211 AA;  24122 MW;  A15B2683C53B2F1C CRC64;

  Query Match             88.8%;  Score 439.5;  DB 1;  Length 211;
  Best Local Similarity   90.9%;  Pred. No. 2.2e-33;
  Matches   90;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          2 ADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              || | ||| | ||||||:||||| |||||||||||| | |||||||||||||:|||||||
Db          1 ADESRDAAGEARPAPAPVRRRSSANYRAYATEPHAKSKKKISASRKLQLKTLMLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99


RESULT 5
TRIC_MOUSE
ID   TRIC_MOUSE     STANDARD;      PRT;   210 AA.
AC   P48787;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Troponin I, cardiac muscle.
GN   Name=Tnni3;
OS   Mus musculus (Mouse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94103233; PubMed=8276817;
RA   Ausoni S., Campione M., Picard A., Moretti P., Vittadello M.,
RA   de Nardi C., Schiaffino S.;
RT   "Structure and regulation of the mouse cardiac troponin I gene.";
RL   J. Biol. Chem. 269:339-346(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD-1; TISSUE=Heart;
RX   MEDLINE=94253083; PubMed=8195157;
RA   Guo X., Wattanapermpool J., Palmiter K.A., Murphy A.M., Solaro R.J.;
RT   "Mutagenesis of cardiac troponin I. Role of the unique NH2-terminal
RT   peptide in myofilament activation.";
RL   J. Biol. Chem. 269:15210-15216(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Troponin I is the inhibitory subunit of troponin, the
CC       thin filament regulatory complex which confers calcium-sensitivity
CC       to striated muscle actomyosin ATPase activity.
CC   -!- SUBUNIT: Binds to actin and tropomyosin.
CC   -!- SIMILARITY: Belongs to the troponin I family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z22784; CAA80459.1; -.
DR   EMBL; U09181; AAA19657.1; -.
DR   EMBL; BC061171; AAH61171.1; -.
DR   PIR; A53805; A53805.
DR   HSSP; P19429; 1J1D.
DR   MGD; MGI:98783; Tnni3.
DR   GO; GO:0006937; P:regulation of muscle contraction; IDA.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Acetylation; Actin-binding; Muscle protein.
FT   INIT_MET      0      0       By similarity.
FT   SITE          80     80      Involved in TNI-TNT interactions.
FT   SITE          97     97      Involved in TNI-TNT interactions.
FT   DOMAIN        32     79      Involved in binding TNC.
FT   DOMAIN        129    150     Involved in binding TNC and actin.
FT   MOD_RES       1      1       N-acetylalanine (By similarity).
SQ   SEQUENCE   210 AA;  24127 MW;  EBAC8888ACA49A1B CRC64;
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  Query Match           88.0%;  Score 435.5;  DB 1;  Length 210;
  Best Local Similarity  88.9%;  Pred. No. 5.1e-33;
  Matches   88;  Conservative    4;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          2 ADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              || ||||| ||:|||||:||||| |||||||||||||||||||||||||||:|||||||
Db          1 ADESSDAAGEPQPAPAPVRRRSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
                :|||||||||||| | |||||||| |||| ||||||||
Db         61 MEREAEERRGEKGRVLRTRCQPLELDGLGFEELQDLCRQ 99


RESULT 6
Q863B6
ID   Q863B6      PRELIMINARY;      PRT;   210 AA.
AC   Q863B6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cardiac troponin I.
GN   Name=TNNI3;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Left ventricle of heart;
RX   MEDLINE=23081463; PubMed=14719702;
RA   Rishniw M., Barr S.C., Simpson K.W., Winand N.J., Wootton J.A.;
RT   "Cloning and sequencing of the canine and feline cardiac troponin I
RT   genes.";
RL   Am. J. Vet. Res. 65:53-58(2004).
DR   EMBL; AY268184; AAP23052.1; -.
DR   HSSP; P19429; 1J1D.
DR   GO; GO:0030484; C:muscle fiber; IEA.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
SQ   SEQUENCE   210 AA;  23882 MW;  7FD96BC80E6A81B6 CRC64;

  Query Match           87.9%;  Score 435;  DB 2;  Length 210;
  Best Local Similarity  91.0%;  Pred. No. 5.7e-33;
  Matches   91;  Conservative    3;  Mismatches    4;  Indels    2;  Gaps    2;

Qy          1 MADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQ 59
              ||| : |||  | |||||:||||| |||||||||||||||||||||||||||:||||||
Db          1 MAD-NDDAAGCPPPAPAPVRRRSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQ 59

Qy         60 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         60 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99


RESULT 7
TRIC_RAT
ID   TRIC_RAT       STANDARD;      PRT;   210 AA.
AC   P23693;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Troponin I, cardiac muscle.
GN   Name=Tnni3; Synonyms=Ctni, Tni;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91105162; PubMed=1988058;
RA   Murphy A.M., Jones L. II, Sims H.F., Strauss A.W.;
RT   "Molecular cloning of rat cardiac troponin I and analysis of troponin
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RT   I isoform expression in developing rat heart.";
RL   Biochemistry 30:707-712(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92037196; PubMed=1935696;
RA   Ausoni S., de Nardi C., Moretti P., Gorza L., Schiaffino S.;
RT   "Developmental expression of rat cardiac troponin I mRNA.";
RL   Development 112:1041-1051(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91359315; PubMed=1886137; DOI=10.1016/0022-2828(91)90050-V;
RA   Martin A.F., Orlowski J.;
RT   "Molecular cloning and developmental expression of the rat cardiac-
RT   specific isoform of troponin I.";
RL   J. Mol. Cell. Cardiol. 23:583-588(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97218094; PubMed=9065755;
RA   Murphy A.M., Thompson W.R., Peng L.F., Jones L.;
RT   "Regulation of the rat cardiac troponin I gene by the transcription
RT   factor GATA-4.";
RL   Biochem. J. 322:393-401(1997).
CC   -!- FUNCTION: Troponin I is the inhibitory subunit of troponin, the
CC       thin filament regulatory complex which confers calcium-sensitivity
CC       to striated muscle actomyosin ATPase activity.
CC   -!- SUBUNIT: Binds to actin and tropomyosin.
CC   -!- SIMILARITY: Belongs to the troponin I family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M57679; AAA63504.1; -.
DR   EMBL; X58499; CAA41402.1; -.
DR   EMBL; M92074; AAA42294.1; -.
DR   EMBL; U77354; AAB52234.1; -.
DR   PIR; A60124; A60124.
DR   PIR; I56441; I56441.
DR   HSSP; P19429; 1J1D.
DR   RGD; 62052; Tnni3.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Acetylation; Actin-binding; Muscle protein.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       N-acetylalanine (By similarity).
FT   SITE         80     80       Involved in TNI-TNT interactions.
FT   SITE         97     97       Involved in TNI-TNT interactions.
FT   DOMAIN       32     79       Involved in binding TNC.
FT   DOMAIN      129    150       Involved in binding TNC and actin.
FT   CONFLICT      7      7       A -> S (in Ref. 3).
FT   CONFLICT    181    181       I -> T (in Ref. 3).
SQ   SEQUENCE   210 AA;  24028 MW;  077C8889F07465CA CRC64;

  Query Match             87.6%;  Score 433.5;  DB 1;  Length 210;
  Best Local Similarity   88.9%;  Pred. No. 7.9e-33;
  Matches   88;  Conservative    4;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          2 ADGSSDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              || ||||| ||:|||||:||||| |||||||||||||||||||||||||||:|||||||
Db          1 ADESSDAAGEPQPAPAPVRRRSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              :|||||||||||||| |||||||| | |||| ||||||||
Db         61 MEREAEERRGEKGRVLSTRCQPLVLDGLGFEELQDLCRQ 99


RESULT 8
TRIC_BOVIN
ID   TRIC_BOVIN     STANDARD;      PRT;   211 AA.
AC   P08057;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Troponin I, cardiac muscle.
GN   Name=TNNI3;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=88294022; PubMed=3042023;
RA   Leszyk J., Dumaswala R., Potter J.D., Collins J.H.;
RT   "Amino acid sequence of bovine cardiac troponin I.";
RL   Biochemistry 27:2821-2827(1988).
RN   [2]
RP   SEQUENCE.
RX   MEDLINE=88240346; PubMed=2967699;
RA   Creutz C.E., Snyder S.L., Husted L.D., Beggerly L.K., Fox J.W.;
RT   "Pattern of repeating aromatic residues in synexin. Similarity to the
RT   cytoplasmic domain of synaptophysin.";
RL   Biochem. Biophys. Res. Commun. 152:1298-1303(1988).
CC   -!- FUNCTION: Troponin I is the inhibitory subunit of troponin, the
CC       thin filament regulatory complex which confers calcium-sensitivity
CC       to striated muscle actomyosin ATPase activity.
CC   -!- SUBUNIT: Binds to actin and tropomyosin.
CC   -!- SIMILARITY: Belongs to the troponin I family.
DR   PIR; A29994; A29994.
DR   HSSP; P19429; 1LXF.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Acetylation; Actin-binding; Direct protein sequencing; Muscle protein;
KW   Phosphorylation.
FT   MOD_RES       1      1       N-acetylalanine.
FT   SITE         81     81       Involved in TNI-TNT interactions.
FT   SITE         98     98       Involved in TNI-TNT interactions.
FT   DOMAIN       33     80       Involved in binding TNC.
FT   DOMAIN      130    150       Involved in binding TNC and actin.
FT   CONFLICT     16     16       P -> M (in Ref. 2).
SQ   SEQUENCE   211 AA;  23922 MW;  6901792F21913710 CRC64;

  Query Match             83.4%;  Score 413;  DB 1;  Length 211;
  Best Local Similarity   87.0%;  Pred. No. 6.6e-31;
  Matches   87;  Conservative    3;  Mismatches    8;  Indels    2;  Gaps    2;

Qy          2 ADGS-SDAAREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQ 59
              || |   | :  ||| |:||||| |||||||||||||||||||||||||:||||||
Db          1 ADRSGGSTAGDTVPAPPPVRRRSSANYRAYATEPHAKKKSKISASRKLQLKTLMLQIAKQ 60

Qy         60 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              ||||||||||||||||||||||||||||||||||||||||
Db         61 ELEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 100


RESULT 9
Q6S7R4
ID   Q6S7R4      PRELIMINARY;      PRT;   208 AA.
AC   Q6S7R4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   High Mr cardiac troponin I.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14736877; DOI=10.1074/jbc.M314225200;
RA   Biesiadecki B.J., Schneider K.L., Yu Z.B., Chong S.M., Jin J.P.;
RT   "An Arg111Cys polymorphism in wild turkey cardiac troponin I
```

```
RT   accompanying the dilated cardiomyopathy-related abnormal splicing
RT   variant of cardiac troponin T with potentially compensatory effects.";
RL   J. Biol. Chem. 279:13825-13832(2004).
DR   EMBL; AY463244; AAS45405.1; -.
DR   GO; GO:0030484; C:muscle fiber; IEA.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
SQ   SEQUENCE   208 AA;  23575 MW;  56345D467938BAB5 CRC64;

  Query Match             61.7%;  Score 305.5;  DB 2;  Length 208;
  Best Local Similarity   68.5%;  Pred. No. 8.1e-21;
  Matches   63;  Conservative    9;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          9 AREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQELEREAEE 67
              | |  | | |:||:|| ||| || |||||::||||||||||||||||| ||:||||| :|
Db          2 AEEEEPKPPPLRRKSSANYRGYAVEPHAKRQSKISASRKLQLKTLLLQRAKRELEREEQE 61

Qy         68 RRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              | ||| | |   | | || ||| |:||:|||:
Db         62 RAGEKQRHLGELCPPPELEGLGVAQLQELCRE 93


RESULT 10
Q6S7R5
ID   Q6S7R5      PRELIMINARY;      PRT;   208 AA.
AC   Q6S7R5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Low Mr cardiac troponin I.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14736877; DOI=10.1074/jbc.M314225200;
RA   Biesiadecki B.J., Schneider K.L., Yu Z.B., Chong S.M., Jin J.P.;
RT   "An Arg111Cys polymorphism in wild turkey cardiac troponin I
RT   accompanying the dilated cardiomyopathy-related abnormal splicing
RT   variant of cardiac troponin T with potentially compensatory effects.";
RL   J. Biol. Chem. 279:13825-13832(2004).
DR   EMBL; AY463243; AAS45404.1; -.
DR   GO; GO:0030484; C:muscle fiber; IEA.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
SQ   SEQUENCE   208 AA;  23628 MW;  A32F5CED638911B4 CRC64;

  Query Match             61.7%;  Score 305.5;  DB 2;  Length 208;
  Best Local Similarity   68.5%;  Pred. No. 8.1e-21;
  Matches   63;  Conservative    9;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          9 AREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQELEREAEE 67
              | |  | | |:||:|| ||| || |||||::||||||||||||||||| ||:||||| :|
Db          2 AEEEEPKPPPLRRKSSANYRGYAVEPHAKRQSKISASRKLQLKTLLLQRAKRELEREEQE 61

Qy         68 RRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              | ||| | |   | | || ||| |:||:|||:
Db         62 RAGEKQRHLGELCPPPELEGLGVAQLQELCRE 93


RESULT 11
Q6S7R6
ID   Q6S7R6      PRELIMINARY;      PRT;   208 AA.
AC   Q6S7R6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cardiac troponin I.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=14736877; DOI=10.1074/jbc.M314225200;
RA   Biesiadecki B.J., Schneider K.L., Yu Z.B., Chong S.M., Jin J.P.;
RT   "An Arg111Cys polymorphism in wild turkey cardiac troponin I
RT   accompanying the dilated cardiomyopathy-related abnormal splicing
RT   variant of cardiac troponin T with potentially compensatory effects.";
RL   J. Biol. Chem. 279:13825-13832(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Jin J.-P., Yu Z.-B.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY463242; AAS45403.1; -.
DR   GO; GO:0030484; C:muscle fiber; IEA.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
SQ   SEQUENCE   208 AA;  23628 MW;  A32F5CED638911B4 CRC64;

  Query Match             61.7%;  Score 305.5;  DB 2;  Length 208;
  Best Local Similarity   68.5%;  Pred. No. 8.1e-21;
  Matches   63;  Conservative    9;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          9 AREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQELEREAEE 67
              | |  | | |:||:|| ||| || |||||::||||||||||||||||| ||:||||| :|
Db          2 AEEEEPKPPPLRRKSSANYRGYAVEPHAKRQSKISASRKLQLKTLLLQRAKRELEREEQE 61

Qy         68 RRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              | ||| | |   | | || ||| |:||:|||:
Db         62 RAGEKQRHLGELCPPPELEGLGVAQLQELCRE 93


RESULT 12
TRIC_COTJA
ID   TRIC_COTJA     STANDARD;      PRT;   207 AA.
AC   P27672;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Troponin I, cardiac muscle.
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92011768; PubMed=1918073;
RA   Hastings K.E., Koppe R.I., Marmur E., Bader D., Shimada Y., Toyota N.;
RT   "Structure and developmental expression of troponin I isoforms. cDNA
RT   clone analysis of avian cardiac troponin I mRNA.";
RL   J. Biol. Chem. 266:19659-19665(1991).
CC   -!- FUNCTION: Troponin I is the inhibitory subunit of troponin, the
CC       thin filament regulatory complex which confers calcium-sensitivity
CC       to striated muscle actomyosin ATPase activity.
CC   -!- SUBUNIT: Binds to actin and tropomyosin.
CC   -!- SIMILARITY: Belongs to the troponin I family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M73702; AAA49513.1; -.
DR   HSSP; P19429; 1J1D.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Acetylation; Actin-binding; Muscle protein.
FT   INIT_MET      0      0       By similarity.
FT   MOD_RES       1      1       N-acetylalanine (By similarity).
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FT   DOMAIN       27     72       Involved in binding TNC.
SQ   SEQUENCE   207 AA;  23470 MW;  D785A518F93E4293 CRC64;

  Query Match           60.9%;  Score 301.5;  DB 1;  Length 207;
  Best Local Similarity   67.4%;  Pred. No. 1.9e-20;
  Matches   62;  Conservative   10;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          9 AREPRPAPAPIRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQELEREAEE 67
              |  |   | | |:||:|| ||| || |||||::|||||||||||||||||| ||::|||| :|
Db          1 AEEEEPKPPPLRRKSSANYRGYAVEPHAKRQSKISASRKLQLKTLLLQRAKRDLEREEQE 60

Qy         68 RRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
                | ||| | |   | | || ||| |:||:|||:
Db         61 RAGEKQRHLGELCPPPELDGLGVAQLQELCRE 92


RESULT 13
Q63ZJ0
ID   Q63ZJ0      PRELIMINARY;      PRT;   246 AA.
AC   Q63ZJ0;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Klein S., Gerhard D.S.;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC082923; AAH82923.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   246 AA;  28333 MW;  685317D78F5D7730 CRC64;

  Query Match           59.9%;  Score 296.5;  DB 2;  Length 246;
  Best Local Similarity   64.6%;  Pred. No. 6.8e-20;
  Matches   64;  Conservative   10;  Mismatches   18;  Indels    7;  Gaps    2;

Qy          8 AAREPRPAPAP------IRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
                |    |:||| |      |||||| |||||||||   | | ||||||||||:|:||||| |
Db         28 APEPPKPAPPPAAPPPLIRRRSSANYRAYATEPQVKIKPKISASRKLQLKSLMLQIAKAE 87

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
                :| | |||  || | |: :||||:|:||  :|||||||:
Db         88 MEHEEEERALEKERYLAEQCQPLQLSGLSLSELQDLCRE 126


RESULT 14
TRIC_XENLA
ID   TRIC_XENLA     STANDARD;      PRT;   243 AA.
AC   P50754;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Troponin I, cardiac muscle (Troponin IC).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart muscle;
RX   MEDLINE=95046865; PubMed=7958411; DOI=10.1006/dbio.1994.1265;
RA   Drysdale T.A., Tonissen K.F., Patterson K.D., Crawford M.J.,
RA   Krieg P.A.;
RT   "Cardiac troponin I is a heart-specific marker in the Xenopus embryo:
RT   expression during abnormal heart morphogenesis.";
RL   Dev. Biol. 165:432-441(1994).
CC   -!- FUNCTION: Troponin I is the inhibitory subunit of troponin, the
CC       thin filament regulatory complex which confers calcium-sensitivity
CC       to striated muscle actomyosin ATPase activity.
CC   -!- SUBUNIT: Binds to actin and tropomyosin.
CC   -!- TISSUE SPECIFICITY: Heart.
CC   -!- DEVELOPMENTAL STAGE: Expressed at all stages of development.
CC   -!- SIMILARITY: Belongs to the troponin I family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; L25721; AAA65727.1; -.
DR   PIR; I51408; I51408.
DR   HSSP; P19429; 1J1D.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Actin-binding; Muscle protein.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        9     14       Poly-Glu.
FT   DOMAIN       17     22       Poly-Glu.
FT   DOMAIN       84     91       Poly-Glu.
SQ   SEQUENCE   243 AA;  28067 MW;  A7CC018ACCB26675 CRC64;

  Query Match           59.5%;  Score 294.5;  DB 1;  Length 243;
  Best Local Similarity   62.6%;  Pred. No. 1e-19;
  Matches   62;  Conservative   12;  Mismatches   18;  Indels    7;  Gaps    2;

Qy          8 AAREPRPAPAP------IRRRSS-NYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
                |   |:||| |      |||||| |||:|||||  |:| ||||||||| |::|||||
Db         25 APEPPKPAPPPAAPPPLIRRRSSANYRSYATEPQVKRKPKISASRKLQLNTMMLQIAKAE 84

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
                :||| |||  || | |:  ||||:|:||  :|||||::
Db         85 MEREEEERAREKERYLAEHCQPLQLSGLSRSELQDLCQE 123
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RESULT 15
Q6YA69
ID   Q6YA69      PRELIMINARY;      PRT;   238 AA.
AC   Q6YA69;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cardiac troponin I.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   PubMed=14745952; DOI=10.1002/dvdy.10434;
RA   Warkman A.S., Atkinson B.G.;
RT   "Amphibian cardiac troponin I gene's organization, developmental
RT   expression, and regulatory properties are different from its mammalian
RT   homologue.";
RL   Dev. Dyn. 229:275-288(2004).
DR   EMBL; AY166834; AAO33937.1; -.
DR   GO; GO:0030484; C:muscle fiber; IEA.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
SQ   SEQUENCE   238 AA;  27415 MW;  A2E1600D35594212 CRC64;

  Query Match             59.3%;  Score 293.5;  DB 2;  Length 238;
  Best Local Similarity   59.4%;  Pred. No. 1.3e-19;
  Matches   57;  Conservative   16;  Mismatches   16;  Indels    7;  Gaps    1;

Qy          11 EPRPAPAPI-------RRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQELER 63
               |  ||| |:       |: |:|||:||||||||:| ||:||||||| |:||||| |:|:
Db          23 EKEPAPPPVTVPPLIRRKSSANYRSYATEPHAKRKPKITASRKLQLKGLMLQIAKHEMEQ 82

Qy          64 EAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
               | | |  || | |: ||:||:|:||  :||||:||:
Db          83 EEEARAQEKERVLAERCEPLQLSGLSISELQDMCRE 118


Search completed: August 30, 2005, 12:11:39
Job time : 170 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2005, 11:49:21 ; Search time 165 Seconds
(without alignments)
232.056 Million cell updates/sec

Title: US-09-941-997-2
Perfect score: 495
Sequence: 1 MADGSSDAAREPRPAPAPIR.....CQPLELAGLGFAELQDLCRQ 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	495	100.0	99	3	AAY87943	Aay87943 Human tro
2	495	100.0	203	6	ABO14732	Abo14732 Novel hum
3	495	100.0	210	2	AAB12185	Aab12185 Human tro
4	495	100.0	210	4	ADT02432	Adt02432 Human Tro
5	495	100.0	210	6	ABO14735	Abo14735 Novel hum
6	495	100.0	210	7	ADJ68246	Adj68246 Human hea
7	495	100.0	210	7	ADJ70547	Adj70547 Human hea
8	495	100.0	211	2	AAY03179	Aay03179 Human car
9	495	100.0	212	2	AAW94061	Aaw94061 Cardiac t
10	495	100.0	216	2	AAW41573	Aaw41573 Modified
11	495	100.0	216	2	AAW72758	Aaw72758 Modified
12	495	100.0	216	3	AAY91087	Aay91087 Recombina
13	495	100.0	216	7	ADG14208	Adg14208 Human tro
14	495	100.0	222	2	AAW41570	Aaw41570 Modified
15	495	100.0	222	6	ABO14731	Abo14731 Novel hum
16	495	100.0	371	7	ADG14211	Adg14211 Human tro
17	495	100.0	390	2	AAY25115	Aay25115 Human car
18	495	100.0	390	7	ADG14206	Adg14206 Human Tro
19	491	99.2	226	2	AAW18054	Aaw18054 Recombina
20	491	99.2	226	2	AAY03174	Aay03174 Recombina
21	491	99.2	226	2	AAY03168	Aay03168 Recombina
22	491	99.2	319	2	AAW41572	Aaw41572 Human car
23	491	99.2	372	2	AAW41571	Aaw41571 Cardiac t
24	490	99.0	209	8	ADO03924	Ado03924 Human ful
25	487	98.4	203	6	ABO14734	Abo14734 Novel hum
26	486	98.2	153	2	AAW18053	Aaw18053 Recombina
27	486	98.2	153	2	AAY03176	Aay03176 Human car
28	486	98.2	153	2	AAY03169	Aay03169 Human car
29	486	98.2	208	2	AAW94064	Aaw94064 Cardiac t
30	486	98.2	209	2	AAY03175	Aay03175 Human car
31	486	98.2	209	2	AAY03167	Aay03167 Human car
32	477.5	96.5	162	4	ABG23116	Abg23116 Novel hum
33	444	89.7	150	2	AAW94063	Aaw94063 Cyanogen
34	435.5	88.0	210	8	ADO03928	Ado03928 Mouse ful
35	435.5	88.0	211	6	ABP98855	Abp98855 Human str
36	433.5	87.6	210	8	ADO03916	Ado03916 Rat full
37	423.5	85.6	229	4	ABG23117	Abg23117 Novel hum
38	413	83.4	211	8	ADO03927	Ado03927 Bovine fu
39	397	80.2	80	2	AAW02286	Aaw02286 Human tro
40	397	80.2	80	2	AAW94062	Aaw94062 Cardiac t
41	395	79.8	80	2	AAY03180	Aay03180 Human car
42	394	79.6	206	8	ADO03925	Ado03925 Rabbit fu
43	356	71.9	247	4	ADT02426	Adt02426 Human Tro
44	356	71.9	264	4	ADT02428	Adt02428 Human Tro
45	331	66.9	178	8	ADS13683	Ads13683 Human car

ALIGNMENTS

RESULT 1
AAY87943
ID AAY87943 standard; protein; 99 AA.
XX
AC AAY87943;
XX
DT 11-SEP-2000 (first entry)
XX
DE Human troponin I protein.
XX
KW Troponin I; human; cardiac; TnI; detection; myocardial infarction;
KW immunodetection; angina; dyspepsia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 20. .30
FT /note= "specifically claimed in Claim 9"
FT Region 95. .115
FT /note= "Specifically claimed in claim 9"
XX
PN WO200023585-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-IB001716.
XX
PR 21-OCT-1998; 98US-00176546.
XX
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
XX
PI Shi Q, Liu S, Ling M;
XX
DR WPI; 2000-422482/36.
DR N-PSDB; AAA39659.
XX
PT New polypeptide useful in assays to identify troponin I associated with
PT cardiac disorders, corresponds to N terminal fragment of human cardiac
PT troponin I.
XX
PS Claim 3; Page 30-31; 34pp; English.
XX
CC This invention describes a novel isolated polypeptide (I) corresponding
CC to an N-terminal fragment of human cardiac troponin I consisting of about
CC 95 to 115 amino acids. Antibodies raised against (I) are useful for the
CC immunodetection of human cardiac troponin I in a bodily fluid, a vital
CC test for suspected acute myocardial infarction, angina and dyspepsia. (I)
CC are used as controls and calibrators for assays which measure the

```
CC   fragments in biological samples. (I) may be used as an affinity matrix
CC   for purifying antibodies from an animal immunized with native troponin I
CC   to isolate those antibodies recognizing epitopes of the fragment. Prior
CC   art assays use different methodologies and components so the
CC   calibrators/controls cannot be used interchangeably among assays. Also,
CC   troponin I in vivo undergoes proteolytic degradation by enzymes present
CC   in the body. (I) is more resistant to proteolysis and is readily
CC   detectable by components of different assays. This sequence represents
CC   the human cardiac troponin I which is described in the method of the
CC   invention
XX
SQ   Sequence 99 AA;

  Query Match             100.0%;  Score 495;  DB 3;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-49;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99


RESULT 2
ABO14732
ID   ABO14732 standard; protein; 203 AA.
XX
AC   ABO14732;
XX
DT   25-AUG-2003  (first entry)
XX
DE   Novel human protein #105.
XX
KW   Human; NOV; gene therapy; endocrine related disease; diabetes;
KW   metabolism-related disease; obesity; central nervous system disorder;
KW   Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;
KW   schizophrenia; depression; autoimmune disorder; inflammatory disorder;
KW   psoriasis; allergy; lupus erythematosus; asthma; cancer;
KW   inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;
KW   colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;
KW   prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;
KW   lung disease; emphysema; obstructive pulmonary disease; haemophilia;
KW   stroke; infection.
XX
OS   Homo sapiens.
XX
PN   WO2003023002-A2.
XX
PD   20-MAR-2003.
XX
PF   09-SEP-2002; 2002WO-US028539.
XX
PR   07-SEP-2001; 2001US-0318120P.
PR   07-SEP-2001; 2001US-0318130P.
PR   10-SEP-2001; 2001US-0318430P.
PR   17-SEP-2001; 2001US-0322636P.
PR   17-SEP-2001; 2001US-0322781P.
PR   17-SEP-2001; 2001US-0322816P.
PR   17-SEP-2001; 2001US-0322817P.
PR   19-SEP-2001; 2001US-0323519P.
PR   20-SEP-2001; 2001US-0323631P.
PR   20-SEP-2001; 2001US-0323636P.
PR   25-SEP-2001; 2001US-0324969P.
PR   25-SEP-2001; 2001US-0325091P.
PR   26-SEP-2001; 2001US-0324990P.
PR   17-APR-2002; 2002US-0373212P.
PR   06-SEP-2002; 2002US-00236177.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;
PI   Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;
PI   Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
PI   Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
PI   Lepley DM, Edinger SR, Burgess CE;
XX
DR   WPI; 2003-313242/30.
DR   N-PSDB; ACD19425.
XX
PT   New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)
PT   and polynucleotides, useful in gene therapy, e.g. for treating or
PT   preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
PT   stroke or infections.
XX
PS   Claim 1; Page 311; 586pp; English.
XX
CC   The invention describes a new isolated polypeptide (NOVX). The NOVX
CC   polypeptide, nucleic acid and antibody are useful as therapeutics,
CC   particularly in the manufacture of a medicament for treating a syndrome
CC   associated with a human disease, which includes a pathology associated
CC   with NOVX polypeptide. The DNA encoding the protein is useful in gene
CC   therapy for treating the disease or condition. In particular, the NOVX
CC   polypeptide or polynucleotide is useful for treating endocrine/
CC   metabolism-related diseases (e.g. obesity or diabetes), central nervous
CC   system disorders (e.g. Alzheimer's disease, Parkinson's disease,
CC   epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune
CC   and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,
CC   asthma, inflammatory bowel disease, rheumatoid arthritis or
CC   osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
CC   prostate or brain cancers, or melanoma), liver diseases (e.g. liver
CC   cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
CC   haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
CC   These are also useful in developing powerful assay system for functional
CC   analysis of various human disorders, as well as in diagnostic
CC   applications, and for monitoring the effects of drugs during clinical
CC   trials. This is the amino acid sequence of a novel human NOV protein
XX
SQ   Sequence 203 AA;

  Query Match             100.0%;  Score 495;  DB 6;  Length 203;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-48;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99


RESULT 3
AAB12185
ID   AAB12185 standard; protein; 210 AA.
XX
AC   AAB12185;
XX
DT   10-NOV-2000  (first entry)
XX
DE   Human troponin I cardiac isoform (cTnI).
XX
KW   Human; troponin I; cTnI; muscle; acute myocardial infarction;
KW   protein subunit stabilisation.
XX
OS   Homo sapiens.
XX
PN   US6072040-A.
XX
PD   06-JUN-2000.
XX
PF   15-OCT-1997;  97US-00950925.
XX
```

PR 15-OCT-1996; 96US-00730111.
XX
PA (MEDI-) MEDICAL ANALYSIS SYSTEMS INC.
XX
PI Sintar E, Dave KI, Botyanszki J;
XX
DR WPI; 1998-251059/22.
DR N-PSDB; AAA62127.
XX
PT Stabilising individual sub-units of multimeric protein by attaching to
PT polymer - particularly cardiac troponin sub-units for use as controls in
PT immunoassays for diagnosis of acute myocardial infarct.
XX
PS Disclosure; Col 13-16; 17pp; English.
XX
CC Troponin is a three-subunit complex of troponin I, T and C. The troponin
CC complex is involved in the calcium-sensitive switch that regulates actin
CC and myosin interaction in striated muscles. The present sequence is the
CC protein sequence of the cardiac isoform of troponin I. cTnI is a specific
CC marker for the diagnosis of acute myocardial infarction. The cTnI protein
CC subunit may be stabilised by covalent conjugation to polymers, where a
CC solution of cTnI is mixed with an active polymer allowing a cTnI-polymer
CC conjugate to be formed. Stabilised conjugates of cTnI are useful as
CC control reagent compositions for immunoassays. The stabilising effect of
CC conjugation allows the individual subunit to be stored in liquid medium
CC for longer periods of time than an equivalent unconjugated or "free"
CC individual subunit
XX
SQ Sequence 210 AA;

Query Match 100.0%; Score 495; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
|||||||||||||||||||||||||||||||||||||
Db 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99

RESULT 4
ADT02432
ID ADT02432 standard; protein; 210 AA.
XX
AC ADT02432;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human Troponin I subunit.
XX
KW Human; Troponin I; Troponin C; antigen; myocardial infarction; cardiant.
XX
OS Homo sapiens.
XX
PN US6475785-B1.
XX
PD 05-NOV-2002.
XX
PF 05-AUG-1999; 99US-00368819.
XX
PR 18-DEC-1997; 97US-00993380.
PR 21-OCT-1998; 98US-00176546.
XX
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
XX
PI Shi Q, Liu S, Ling M;
XX
DR WPI; 2001-202771/20.
XX
PT Single-chain polypeptides comprising an N-terminal fragment of cardiac
PT troponin I and cardiac troponin C, useful as controls or calibrators for
PT troponin assays.
XX
PS Disclosure; SEQ ID NO 8; 11pp; English.
XX
CC The invention relates to a single-chain polypeptide comprising a N-
CC terminal fragment of cardiac troponin I and a cardiac troponin C. The
CC presence of cardiac troponin subunits (I, C or T) in the bloodstream is a
CC marker for myocardial infarction. Also included are a polynucleotide
CC encoding the polypeptide, a replicatable cloning or expression vehicle
CC comprising the polynucleotide, a host cell transformed with the
CC expression vehicle, a composition (comprising the polypeptide) for use as
CC a control or calibrator for a troponin I assay and quantitating troponin
CC I in a sample (by measuring troponin I in the sample, measuring the
CC fusion protein in a standard having a known quantity of troponin I, and
CC correlating the troponin I measured in the sample with the known quantity
CC of troponin I measured in the standard, to provide the quantity of
CC troponin I in the sample). The single-chain polypeptide is useful as a
CC control or calibrator for a troponin I assay and for affinity
CC purification of troponin antibodies. The present sequence represents
CC human troponin I subunit. NOTE: The present sequence is included in the
CC sequence listing but is not mentioned anywhere else in the specification.
CC The identity of the sequence was determined by the indexer via BLAST
CC searching and by comparison to ADT02426, where the sequence was found to
CC be 100% identical to human Troponin I and matched the N-terminus of
CC ADT02426.
XX
SQ Sequence 210 AA;

Query Match 100.0%; Score 495; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
|||||||||||||||||||||||||||||||||||||
Db 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99

RESULT 5
ABO14735
ID ABO14735 standard; protein; 210 AA.
XX
AC ABO14735;
XX
DT 25-AUG-2003 (first entry)
XX
DE Novel human protein #108.
XX
KW Human; NOV; gene therapy; endocrine related disease; diabetes;
KW metabolism-related disease; obesity; central nervous system disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;
KW stroke; infection.
XX
OS Homo sapiens.
XX
PN WO2003023002-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028539.
XX
PR 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318130P.

PR 10-SEP-2001; 2001US-0318430P.
PR 17-SEP-2001; 2001US-0322636P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 17-SEP-2001; 2001US-0322817P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 17-APR-2002; 2002US-0373212P.
PR 06-SEP-2002; 2002US-00236177.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;
PI Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;
PI Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
PI Lepley DM, Edinger SR, Burgess CE;
XX
DR WPI; 2003-313242/30.
DR N-PSDB; ACD19428.
XX
PT New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)
PT and polynucleotides, useful in gene therapy, e.g. for treating or
PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
PT stroke or infections.
XX
PS Claim 1; Page 312; 586pp; English.
XX
CC The invention describes a new isolated polypeptide (NOVX). The NOVX
CC polypeptide, nucleic acid and antibody are useful as therapeutics,
CC particularly in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, which includes a pathology associated
CC with NOVX polypeptide. The DNA encoding the protein is useful in gene
CC therapy for treating the disease or condition. In particular, the NOVX
CC polypeptide or polynucleotide is useful for treating endocrine/
CC metabolism-related diseases (e.g. obesity or diabetes), central nervous
CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,
CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune
CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,
CC asthma, inflammatory bowel disease, rheumatoid arthritis or
CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver
CC cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
CC haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
CC These are also useful in developing powerful assay system for functional
CC analysis of various human disorders, as well as in diagnostic
CC applications, and for monitoring the effects of drugs during clinical
CC trials. This is the amino acid sequence of a novel human NOV protein
XX
SQ Sequence 210 AA;

```
  Query Match             100.0%;  Score 495;  DB 6;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-48;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
```

RESULT 6
ADJ68246
ID ADJ68246 standard; protein; 210 AA.
XX
AC ADJ68246;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID52.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 52; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 210 AA;

```
  Query Match             100.0%;  Score 495;  DB 7;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-48;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
```

RESULT 7
ADJ70547

```
ID   ADJ70547 standard; protein; 210 AA.
XX
AC   ADJ70547;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID2353.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2003087768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS,  Fahy ED,  Zhang B,  Gibson BW,  Taylor SW,  Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 2353; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 210 AA;

  Query Match             100.0%;  Score 495;  DB 7;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-48;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
```

```
RESULT 8
AAY03179
ID   AAY03179 standard; peptide; 211 AA.
XX
AC   AAY03179;
XX
DT   15-JUN-1999  (first entry)
XX
DE   Human cardiac troponin I fragment.
XX
KW   Human; cardiac troponin I; TnI; diagnostic calibrator; troponin assay.
XX
OS   Homo sapiens.
XX
PN   WO9854219-A1.
XX
PD   03-DEC-1998.
XX
PF   21-MAY-1998;   98WO-US010518.
XX
PR   29-MAY-1997;   97US-00865468.
PR   13-JUN-1997;   97US-00874566.
PR   22-JUL-1997;   97US-00898649.
XX
PA   (MEDI-) MEDICAL ANALYSIS SYSTEMS INC.
XX
PI   Moriana N;
XX
DR   WPI; 1999-059811/05.
XX
PT   New compositions comprising complexes of cardiac troponin I or T - useful
PT   as diagnostic calibrators, or controls or reference material for TnI or
PT   TnT.
XX
PS   Disclosure; Page 18; 50pp; English.
XX
CC   This sequence represents a human cardiac troponin I (TnI) fragment. The
CC   invention relates to compositions used in an assay for determining the
CC   presence/concentration of TnI or TnT. The compositions comprise a complex
CC   of either/both TnI or TnT (including fragments), covalently bound to TnC
CC   (including fragments) or each other. The complexes are useful as
CC   diagnostic calibrators or controls in methods for assaying each troponin
CC   (especially TnI and TnT), and they are also useful as reference materials
CC   for TnI and TnT. The compositions possess higher stability and/or
CC   immunoreactivity over prior art complexes and analytes
XX
SQ   Sequence 211 AA;

  Query Match             100.0%;  Score 495;  DB 2;  Length 211;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-48;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
```

```
RESULT 9
AAW94061
ID   AAW94061 standard; peptide; 212 AA.
XX
AC   AAW94061;
XX
DT   09-APR-1999  (first entry)
XX
DE   Cardiac troponin I (cTnI) protein fragment.
XX
KW   Myoglobin; troponin; anoxia; antioxidant; clinical assay; TnI; TnT; TnC;
```

KW calcium; stabilise; cardiac marker; cardiac; lyophilisate;
KW cardiac troponin I; cTnI; human; bovine.
XX
OS Homo sapiens.
OS Bos sp.
XX
PN WO9856900-A1.
XX
PD 17-DEC-1998.
XX
PF 09-JUN-1998; 98WO-US011809.
XX
PR 13-JUN-1997; 97US-00874566.
PR 22-JUL-1997; 97US-00898538.
XX
PA (MEDI-) MEDICAL ANALYSIS SYSTEMS INC.
XX
PI Palmer DD, Morjana N;
XX
DR WPI; 1999-070321/06.
XX
PT Stabilised control solutions for clinical analysis of cardiac markers -
PT containing one or more of myoglobin, troponins, creatine kinase and
PT carbonic anhydrase, for diagnosis of cardiac function.
XX
PS Disclosure; Page 16; 55pp; English.
XX
CC The invention relates to stabilised compositions for use in clinical
CC assays. Composition to stabilise myoglobin consists of an aqueous
CC buffered solution of myoglobin and can be used for maintaining anoxia and
CC antioxidants. Composition for clinical assays to stabilise troponin I
CC (TnI) or troponin T (TnT) comprises (i) TnI or TnT, (ii) TnC (at least
CC equimolar to (i)) and (iii) calcium ions; wherein the composition is
CC stabilised through a heat treatment process. The compositions are used to
CC analyse for various cardiac markers (for diagnosis of cardiac function),
CC specifically as a control for assay of myoglobin and as control or stock
CC solution for assay of Tn. In these formulations, the cardiac proteins are
CC stabilised, e.g. myoglobin is stable for at least 1 year at 4 deg. C. In
CC the Tn-containing compositions, the heating step and the use of excess
CC TnC both contribute to stability, and several different cardiac proteins
CC may be stabilised in the same solution (which may also be stored as
CC lyophilisate). The present sequence represents cardiac troponin I (cTnI)
CC fragment that can be recombinantly obtained from human cTnI or bovine
CC cTnI
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 495; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
Db 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
Db 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99

RESULT 10
AAW41573
ID AAW41573 standard; protein; 216 AA.
XX
AC AAW41573;
XX
DT 22-JUN-1998 (first entry)
XX
DE Modified human cardiac troponin I HcTnI-(HL)3.
XX
KW Troponin I; immunoassay; assay; analysis; human; cardiac muscle;
KW skeletal muscle; injury; myocardial infarction; diagnosis; HcTnI-(HL)3.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Protein 1. .210
FT /label= HcTnI
FT Peptide 211. .216
FT /label= (HL)3
FT /note= "(Claim 23)"
XX
PN WO9739132-A1.
XX
PD 23-OCT-1997.
XX
PF 14-APR-1997; 97WO-US006147.
XX
PR 16-APR-1996; 96US-0015772P.
PR 11-APR-1997; 97US-00833743.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Potter JD;
XX
DR WPI; 1998-062676/06.
DR N-PSDB; AAV04230.
XX
PT Immunoassay of mammalian troponin using stable standard for comparison -
PT specifically acid-dialysed solution or its lyophilisate used for
PT diagnosis of cardiac or skeletal muscle damage.
XX
PS Example 5; Page 74-75; 94pp; English.
XX
CC This polypeptide comprises a C-terminally modified cardiac troponin I
CC protein, designated HcTnI-(HL)3, comprising human cardiac troponin I
CC (HcTnI) modified to add an alternating 3 histidine 3 leucine tag (see
CC AAW41569). This modification alters the isoelectric point of the protein,
CC thereby improving its solubility and stability. A polynucleotide (see
CC AAV04230) encoding the modified HcTnI was produced by PCR amplification
CC of a HcTnI cDNA template, and was inserted into vector pET 11d to allow
CC expression of HcTnI-(HL)3 in Escherichia coli transformants. The
CC invention provides an assay for measuring mammalian, preferably human,
CC troponin in a patient sample. The assay involves comparing the level in
CC the sample with a novel troponin protein standard. This is a storage
CC stable, soluble troponin, a functional fragment of the troponin, a
CC modified troponin or its functional fragment, a troponin fusion protein
CC or a hetero- multimeric troponin complex (see AAW41570-75). The method is
CC used to monitor changes in the level of human troponin, particularly for
CC diagnosis of diseases involving damage to heart or skeletal muscle, e.g.
CC acute myocardial infarction. It may also be used to study normal and
CC pathological functions of troponin-expressing tissues
XX
SQ Sequence 216 AA;

Query Match 100.0%; Score 495; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
Db 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
Db 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99

RESULT 11
AAW72758
ID AAW72758 standard; protein; 216 AA.
XX
AC AAW72758;
XX
DT 13-JAN-1999 (first entry)

XX
DE Modified human cardiac troponin I.
XX
KW Human cardiac troponin I; troponin T; modified; antigen;
KW stable troponin subunit; cardiac disorder; myocardial damage;
KW heart attack.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5834210-A.
XX
PD 10-NOV-1998.
XX
PF 31-OCT-1997; 97US-00961858.
XX
PR 23-MAY-1997; 97US-00862613.
XX
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
XX
PI Shi Q, Liu S;
XX
DR WPI; 1999-008702/01.
DR N-PSDB; AAV67262.
XX
PT Recombinant modified human cardiac troponin I and complexes with troponin
PT T and C - for use in assays to determine levels of these proteins, as
PT control values in determining extent of cardiac damage e.g. in heart
PT attacks.
XX
PS Claim 2; Fig 1; 16pp; English.
XX
CC The present sequence represents modified human cardiac troponin I.
CC Expression in Escherichia coli of the modified troponin I is increased
CC compared to that of the native sequence. The modified troponin I consists
CC of the native troponin I protein sequence with an N-terminal extension of
CC 5-8 residues, including an N-terminal methionine. The present invention
CC describes troponin protein complexes which are useful for the
CC determination of myocardial damage. Troponin I and troponin T have been
CC found to be highly specific markers for cardiac disorders, especially
CC heart attacks. They must be complexed with troponin C to form a stable
CC structure, which is difficult to isolate. Recombinant preparation of the
CC trimeric structure allows sufficient quantities to be obtained, so that
CC assays can be performed to accurately determine quantification of
CC troponin complex levels for e.g. control values. The complex can also be
CC used as an antigen to raise antibodies
XX
SQ Sequence 216 AA;

Query Match 100.0%; Score 495; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
Db 7 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 66

Qy 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
Db 67 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 105

RESULT 12
AAY91087
ID AAY91087 standard; protein; 216 AA.
XX
AC AAY91087;
XX
DT 08-SEP-2000 (first entry)
XX
DE Recombinant modified human cardiac troponin I SEQ ID NO:5.
XX
KW Human; cardiac troponin I; cardiac troponin T; modified.
XX
OS Homo sapiens.
XX
PN US6060278-A.
XX
PD 09-MAY-2000.
XX
PF 02-JUN-1998; 98US-00089593.
XX
PR 23-MAY-1997; 97US-00862613.
PR 31-OCT-1997; 97US-00961858.
XX
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
XX
PI Shi Q, Liu S;
XX
DR WPI; 2000-364418/31.
DR N-PSDB; AAA39301, AAA39302.
XX
PT Preparing recombinant troponin subunit complexes useful for antibody
PT preparation and troponin assays, involves expressing subunits
PT recombinantly and mixing in aqueous medium containing alkaline earth
PT salt.
XX
PS Claim 6; Fig 1; 16pp; English.
XX
CC The present invention describes the in-vitro preparation of a recombinant
CC troponin C-troponin T-troponin I complex. The troponin complexes from the
CC present invention are useful as antigens to prepare antibodies and as
CC controls and calibrators for troponin assays. The troponin complexes show
CC superior stability and purity and can be utilised as controls among
CC different troponin assay procedures. The production of recombinant human
CC cardiac troponin complexes is independent of the availability of human
CC cardiac tissue and the purification of the complexes is easy. The present
CC sequence is a recombinant modified human cardiac troponin I which is used
CC in the exemplification of the present invention
XX
SQ Sequence 216 AA;

Query Match 100.0%; Score 495; DB 3; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
Db 7 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 66

Qy 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
Db 67 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 105

RESULT 13
ADG14208
ID ADG14208 standard; protein; 216 AA.
XX
AC ADG14208;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human troponin C.
XX
KW linker peptide; troponin I; troponin C; fusion protein;
KW myocardial infarction; heart attack; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003176655-A1.
XX
PD 18-SEP-2003.
XX
PF 28-JAN-2003; 2003US-00353826.

XX
PR 10-DEC-1999; 99US-00458770.
XX
PA (SHIQ/) SHI Q.
PA (SONG/) SONG Q.
XX
PI Shi Q, Song Q;
XX
DR WPI; 2003-898591/82.
DR N-PSDB; ADG14207.
XX
PT New genetic sequence that codes for a single-chain polypeptide comprises
PT cardiac troponin I and troponin C useful for purifying proteins and other
PT substances including antibodies with an affinity for binding troponin I
PT and troponin C.
XX
PS Disclosure; SEQ ID NO 6; 18pp; English.
XX
CC The invention relates to a genetic sequence, which codes for a single-
CC chain polypeptide, comprising cardiac troponin I and troponin C
CC (appearing as ADG14205 encoding ADG14206) separated by a synthetic
CC linker. Also included are a replicatable cloning or expression vehicle
CC comprising the novel genetic sequence, a host cell transformed with the
CC vehicle, an Escherichia coli transformed with the replicatable cloning or
CC expression vehicle and a single-chain polypeptide comprising cardiac
CC troponin I and C. The genetic sequence is useful for purifying proteins
CC and other substances including antibodies with an affinity for binding
CC troponin I and troponin C, for use in diagnostic tests for myocardial
CC infarction (heart attack). The present sequence represents troponin C.
XX
SQ Sequence 216 AA;

Query Match 100.0%; Score 495; DB 7; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
Db 7 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 66

Qy 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
Db 67 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 105

RESULT 14
AAW41570
ID AAW41570 standard; protein; 222 AA.
XX
AC AAW41570;
XX
DT 22-JUN-1998 (first entry)
XX
DE Modified human cardiac troponin I HcTnI-K6-H5-D.
XX
KW Troponin I; immunoassay; assay; analysis; human; cardiac muscle;
KW skeletal muscle; injury; myocardial infarction; diagnosis; HcTnI-K6-H5-D.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9739132-A1.
XX
PD 23-OCT-1997.
XX
PF 14-APR-1997; 97WO-US006147.
XX
PR 16-APR-1996; 96US-0015772P.
PR 11-APR-1997; 97US-00833743.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Potter JD;

XX
DR WPI; 1998-062676/06.
DR N-PSDB; AAV04221.
XX
PT Immunoassay of mammalian troponin using stable standard for comparison -
PT specifically acid-dialysed solution or its lyophilisate used for
PT diagnosis of cardiac or skeletal muscle damage.
XX
PS Example 2; Page 64-65; 94pp; English.
XX
CC This polypeptide comprises a C-terminally modified cardiac troponin I
CC protein, designated HcTnI-K6-H5-D, comprising human cardiac troponin I
CC (HcTnI) modified to add 6 lysines, 5 histidines and one aspartate
CC residue. This modification was made to alter the isoelectric point of the
CC protein, thereby improving its solubility and stability. A polynucleotide
CC (see AAV04221) encoding the modified HcTnI was produced by PCR
CC amplification of a HcTnI cDNA template, and was inserted into vector pET
CC 11d to allow expression of HcTnI-K6-H5-D in Escherichia coli
CC transformants. The invention provides an assay for measuring mammalian,
CC preferably human, troponin in a patient sample. The assay involves
CC comparing the level in the sample with a novel troponin protein standard.
CC This is a storage stable, soluble troponin, a functional fragment of the
CC troponin, a modified troponin or its functional fragment, a troponin
CC fusion protein or a hetero- multimeric troponin complex (see AAW41570-
CC 75). The method is used to monitor changes in the level of human
CC troponin, particularly for diagnosis of diseases involving damage to
CC heart or skeletal muscle, e.g. acute myocardial infarction. It may also
CC be used to study normal and pathological functions of troponin-expressing
CC tissues
XX
SQ Sequence 222 AA;

Query Match 100.0%; Score 495; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
Db 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
Db 61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99

RESULT 15
ABO14731
ID ABO14731 standard; protein; 222 AA.
XX
AC ABO14731;
XX
DT 25-AUG-2003 (first entry)
XX
DE Novel human protein #104.
XX
KW Human; NOV; gene therapy; endocrine related disease; diabetes;
KW metabolism-related disease; obesity; central nervous system disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;
KW stroke; infection.
XX
OS Homo sapiens.
XX
PN WO2003023002-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028539.

```
XX
PR   07-SEP-2001; 2001US-0318120P.
PR   07-SEP-2001; 2001US-0318130P.
PR   10-SEP-2001; 2001US-0318430P.
PR   17-SEP-2001; 2001US-0322636P.
PR   17-SEP-2001; 2001US-0322781P.
PR   17-SEP-2001; 2001US-0322816P.
PR   17-SEP-2001; 2001US-0322817P.
PR   19-SEP-2001; 2001US-0323519P.
PR   20-SEP-2001; 2001US-0323631P.
PR   20-SEP-2001; 2001US-0323636P.
PR   25-SEP-2001; 2001US-0324969P.
PR   25-SEP-2001; 2001US-0325091P.
PR   26-SEP-2001; 2001US-0324990P.
PR   17-APR-2002; 2002US-0373212P.
PR   06-SEP-2002; 2002US-00236177.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;
PI   Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;
PI   Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
PI   Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
PI   Lepley DM, Edinger SR, Burgess CE;
XX
DR   WPI; 2003-313242/30.
DR   N-PSDB; ACD19424.
XX
PT   New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)
PT   and polynucleotides, useful in gene therapy, e.g. for treating or
PT   preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
PT   stroke or infections.
XX
PS   Claim 1; Page 311; 586pp; English.
XX
CC   The invention describes a new isolated polypeptide (NOVX). The NOVX
CC   polypeptide, nucleic acid and antibody are useful as therapeutics,
CC   particularly in the manufacture of a medicament for treating a syndrome
CC   associated with a human disease, which includes a pathology associated
CC   with NOVX polypeptide. The DNA encoding the protein is useful in gene
CC   therapy for treating the disease or condition. In particular, the NOVX
CC   polypeptide or polynucleotide is useful for treating endocrine/
CC   metabolism-related diseases (e.g. obesity or diabetes), central nervous
CC   system disorders (e.g. Alzheimer's disease, Parkinson's disease,
CC   epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune
CC   and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,
CC   asthma, inflammatory bowel disease, rheumatoid arthritis or
CC   osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
CC   prostate or brain cancers, or melanoma), liver diseases (e.g. liver
CC   cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
CC   haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
CC   These are also useful in developing powerful assay system for functional
CC   analysis of various human disorders, as well as in diagnostic
CC   applications, and for monitoring the effects of drugs during clinical
CC   trials. This is the amino acid sequence of a novel human NOV protein
XX
SQ   Sequence 222 AA;

  Query Match             100.0%;  Score 495;  DB 6;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-48;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKSKISASRKLQLKTLLLQIAKQE 60

Qy         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99
              |||||||||||||||||||||||||||||||||||||||
Db         61 LEREAEERRGEKGRALSTRCQPLELAGLGFAELQDLCRQ 99


Search completed: August 30, 2005, 12:05:55
Job time : 167 secs
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